

## Alpha Virus nsp3 alignment

### CLUSTAL W (1.82) multiple sequence alignment

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SFV_nsp3      APSYRVKRDIATCTEAAVVNAANARGTVGDGVCRAVAKKWPSAFKGAATPVGTIKTVMC 60
ONV_nsp3      APSYRVKRMDIAKNTEECVVNAANPRGVPDGVCKAVYRKWPESFRNSATPVGTAKTIMC 60
RRV_nsp3      APSYRVRRDISGHAEAEVVNAANAKGTVGVCRAVARKWPDSFKGAATPVGTAKLVQA 60
SinV_nsp3     APSYRTKRENIADCQEEAVVNAANPLGRPGEVCRAIYKRWPTSFTDSATETGTARMTVC 60
VEEV_nsp3     APSYHVVRGDIATATEGVIINAANSKGQPGGGVCGALYKKFPESFDLQPIEVGKARLVKG 60
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SFV_nsp3      GSYPIHIAVAPNFSATTEAEGDRELAAYRAVAEAVNRLSLSSVAIPLLSTGVFSGGRDR 120
ONV_nsp3      GQYPVIAVAGPNFSNYSEAEGDRELASVYREVAKEVSRLGVSSVAIPLLSTGVYSGGKDR 120
RRV_nsp3      NGMNVIAVAGPNFSTVTEAEGDRELAAYRAVAGIINASNIKSVAIPLLSTGVFSGGKDR 120
SinV_nsp3     LGKKVIAVAGPDRFKHPEAEALKLLQNAVHADVNEHNIKSVAIPLLSTGIYAAGKDR 120
VEEV_nsp3     AAKHIIHAVGPNFNKVSEVEGDKQLAEAYESIATIVNDNNYKSVAIPLLSTGIFSGNKDR 120
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SFV_nsp3      LQQSLNHLFTAMDATDADVTIYCRDKSWEKKIQEAIDMRTAV-ELLNDD----VELTTDL 175
ONV_nsp3      LLQSLNHLFAAMDSTDADVVIYCRDKWEKKITEAISLRSQV-ELLDDH----ISVDCDI 175
RRV_nsp3      VMQSLNHLFTAMDTTDADVVIYCRDKAWKKEKKIQEAIDRRTAV-ELVSED----ISLES DL 175
SinV_nsp3     LEVSLNCLTTALDRTDADVTIYCLDKKWKERIDAALQLKESVTELKDED---MEIDDEL 176
VEEV_nsp3     LTQSLNHLTALDRTDADVAIYCRDKKWEMTLKEAVARREAVEEICISDDSSVTEPD AEL 180
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SFV_nsp3      VRVHPDSSLVGRKGYSTTDGSLYSYFEGTKFKNQAAIDMAEILTLWPRLQEANERICLYAL 235
ONV_nsp3      VRVHPDSSLAGRKGYSTVEGALYSYLEGTRFHQTAVDMAEIIYTMWPKQTEANEQVCLYAL 235
RRV_nsp3      IRVHPDSCLVGRKGYSTITDGKLHSYLEGTRFHQTAVDMAEISTLWPKLQDANEQICLYAL 235
SinV_nsp3     VWIHPDSCLVGRKGFSTTKGKLYSYFEGTKFQHQAADMAEIKVLFPPNDQESNEQLCAYIL 236
VEEV_nsp3     VRVHPKSSLAGRKGYSTSDGKTFSYLEGTKFQHQAADIAEINAMWVPVATEANEQVCMYIL 240
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SFV_nsp3      GETMDNIGSKCPVNDSDSSTPPRTVPCLCRYAMTAERLARLRSHQVKSMMVCSFPLPKY 295
ONV_nsp3      GESIESVRQKCPVDDADASFPPKTVPCLCRYAMTPERVARLRMNHTTSIIVCSSFPLPKY 295
RRV_nsp3      GESMDSIRTKCPVEDADSSTPPKTVPCLCRYAMTAERVARLRMNNTKAIIVCSFPLPKY 295
SinV_nsp3     GETMEAIREKCPVDHNPSSPPKTLPCLCMYAMTPERVHRLRSNNVKEVTVCSSTPLPKH 296
VEEV_nsp3     GESMSSIRSKCPVEESEASTPPSTLPCLCIHAMTPERVQRLKASRPEQITVCSSFPLPKY 300
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SFV_nsp3      HVDGVQKVKCEKVLLEFDPTVPSVSPRKYAAS-----TTDHSDRSLRGFDLDWTTDSSST 350
ONV_nsp3      KIEGVQKVKCSKALLEFDHNVPSPRVSPRTYRPADEIIQTPQTPTEACQDAQLVQSINDEAV 355
RRV_nsp3      RIEGVQKVKCDRVLIFDQTVPSLVSPRKYIPAAASMHADTVSLDSTVSTGSAWSFPSEAT 355
SinV_nsp3     KIKNVQKVQCTKVVLNPHPTPAFVPARKYIEVPE---OPTAPPAQAEAEPEVVATPSPST 353
VEEV_nsp3     RITGVQKIQCSQPILFSPKVPAYIHPRKYLVEVTPVEETPESPAENQSTEGTPEQPALVN 360
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SFV_nsp3      -----ASDTMSLPSLQSCDIDSIEPMAPE-----IVVTADVHP-----EPAGI 388
ONV_nsp3      PVPSDLEACDATMDWPSIGTVSTRQRHDSSDSEYSGRSNIQLVTADVHAPMYAHS LASS 415
RRV_nsp3      -YETMEVVAEVVHSEPPVPPPRRRRAQVTMHH-----QELLEVS DMHT-----PIAAR 402
SinV_nsp3     ADNTSLDVTDISLDMDDSSSEGLFSFSGSDN-----SITSMDSW-----SGPSS 399
VEEV_nsp3     VDATRTRMPEPIIIIEEEEEDSISLLSDGPTHQ-----VLQVEADIHG-----SPSVS 407
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SFV_nsp3      ADLAADVHPEPADH-----VDLEN-----PIPPRPKRAAYLASRAAER----- 427
ONV_nsp3      GGSMLSLSSEPAQNGTMILLDSED TDSISRSTPIAPPRRLGRTINVTCDERE--GKIL 473
RRV_nsp3      VEIPVYDTAVVAER-VAIPCTSEY-----ATPIPTPRAVRVVPVPAPRIQRASTYRVS 454
SinV_nsp3     LEIVDRRQVVVADV----HAVQEP-----APIPPRLKKMARLAAARKEPTPPASNS 447
VEEV_nsp3     SSSWSIPHASDFDVSLSILDTLDG-----ASVTSGAVSAETNSYFARSMEFRAR 457
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SFV_nsp3      PVPAPR-KPTPAPRTAFR-----NKLPLTFGDFDEHEVDAL-- 462
ONV_nsp3      PMASDR-FFTAKPYTVALSVSTADMTVYPIQAPLGLIPPTLEPITFGDFAEGEIDNL-- 530
RRV_nsp3      PTPTPR-VLRASVCSVTTSAG----VEFPWAPEDLEVLPVHCEMREPVELPWEPE-- 506
SinV_nsp3     SESLHL-SFGGVSMGLGSIFDG---ETARQAQVPLATGPTDVPMSFGSFGSDGEIDELSR 503
VEEV_nsp3     PVPAPRTVFRNPPHPAPRTRTP----PLAHSRASSRTSLVSTPPGVNRVITREELEALTP 513
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SFV_nsp3      ---ASG-ITFGDF-----DDVRLRLGRAGA--- 482
ONV_nsp3      ---LTGALTFGDFEPGEVEELTDSEWSTCSDTDEELRLDRAGG--- 570
RRV_nsp3      ---DVD-IQFGDFET-----PDKIQFGDIDFDQF 531
SinV_nsp3     RVTSESPVLFGSFEPGEVNSIISSRSAVSFPLRKQRRRRRSRTEY 549
VEEV_nsp3     SRAPSRASRTSLVS-----NPPGVNRVITREEFEAFVAQQQ-- 550
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